

**Figure 1**

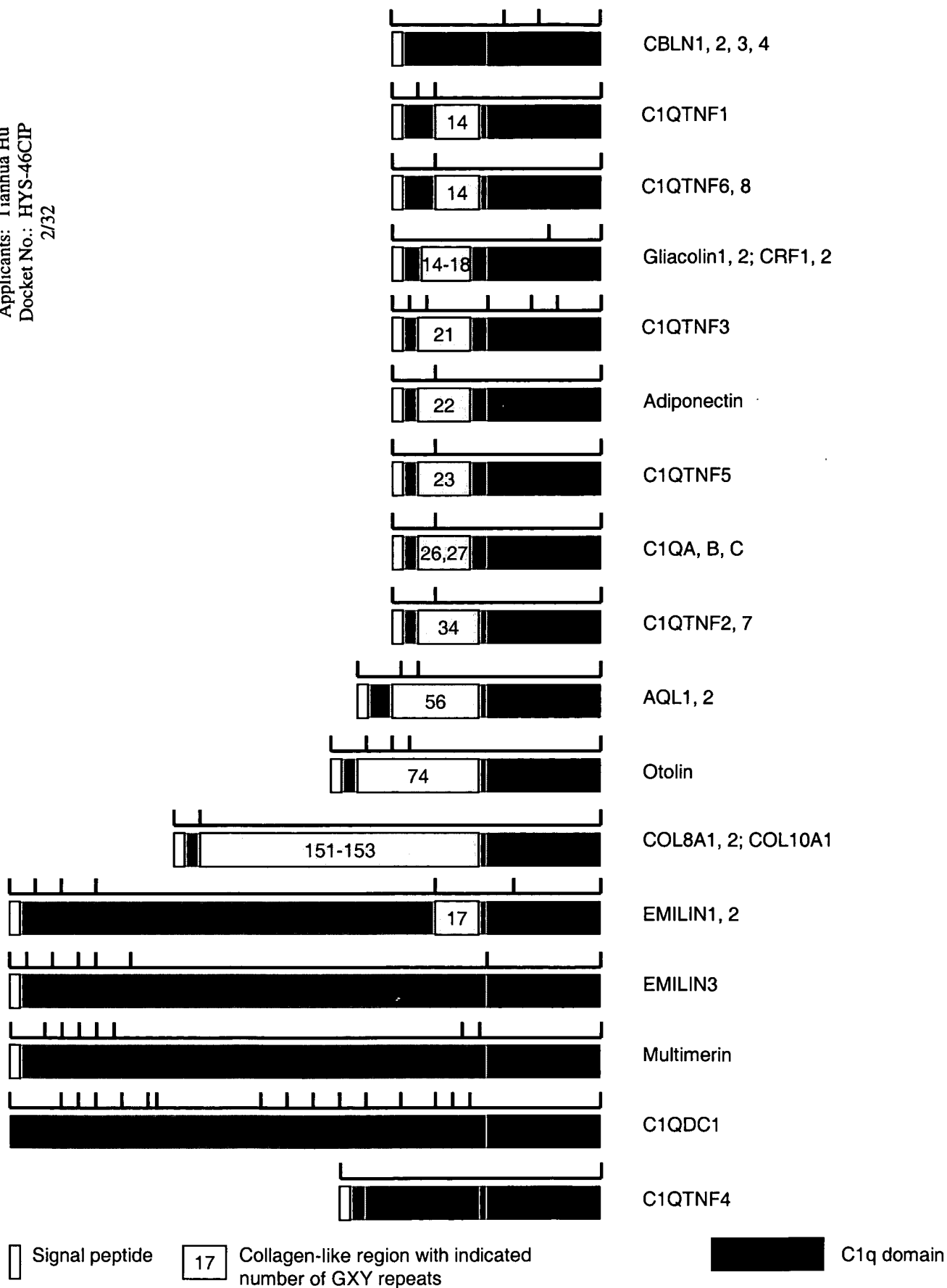


Figure 2

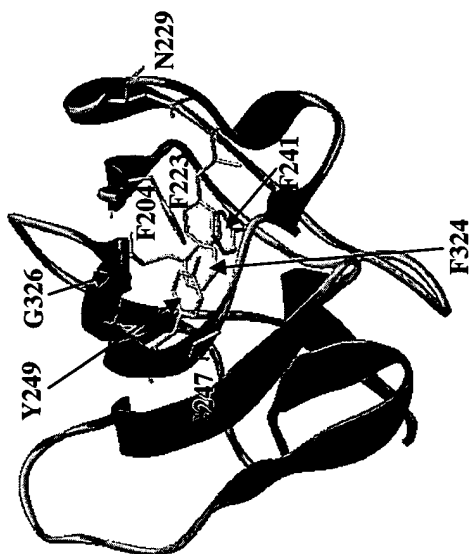
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
3/32

Figure 3A

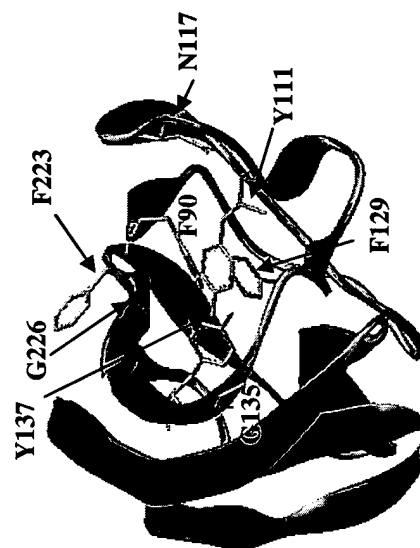


Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
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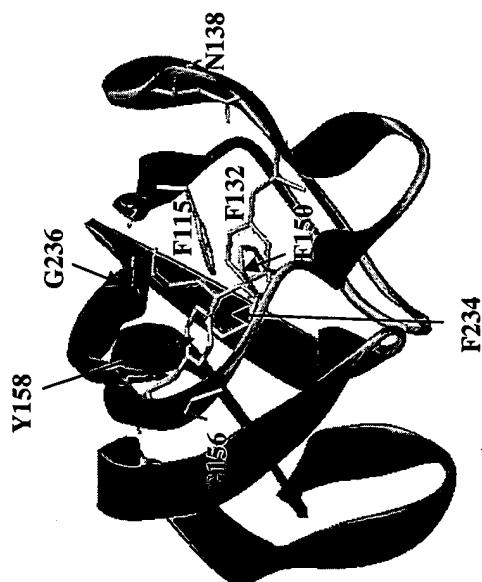
AQL1



CV34-23



Adiponectin



C1qTNF7

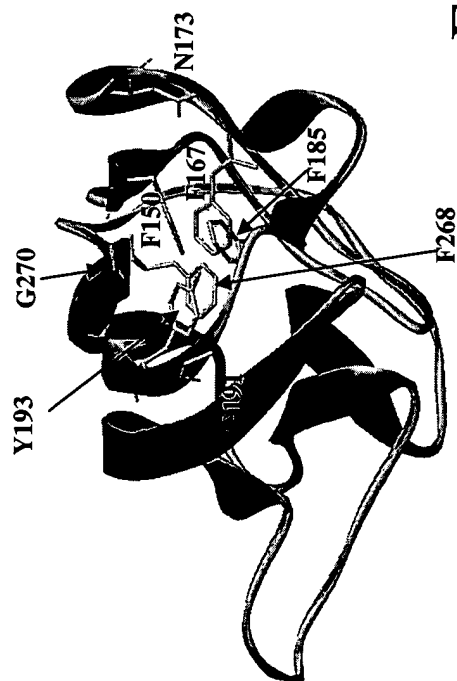


Figure 4

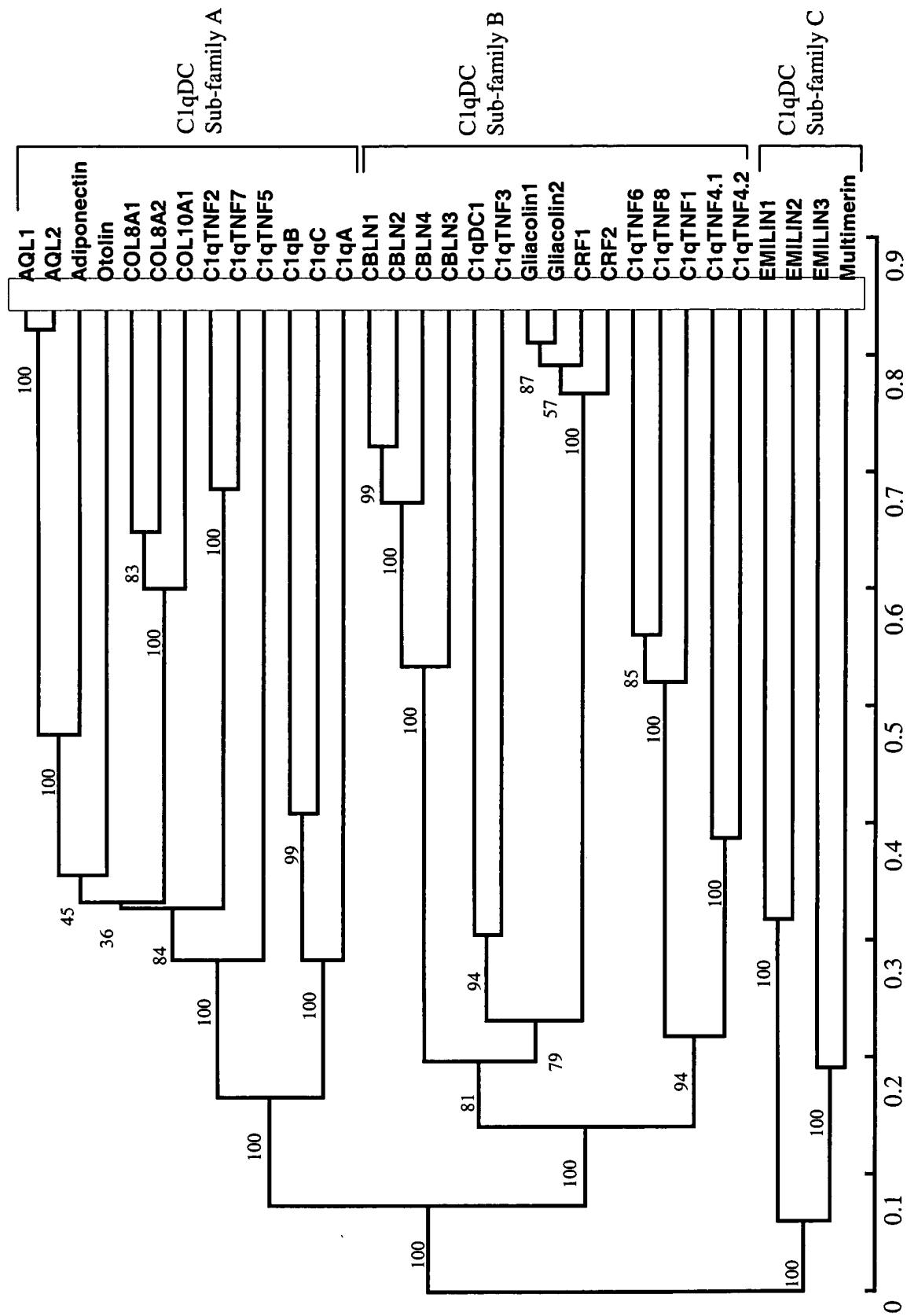


Figure 5

CLUSTAL W MULTIPLE SEQUENCE ALIGNMENT OF  
ADIPONECTIN-LIKE CDCP POLYPEPTIDES (SEQ ID NOS: 4,  
7, 10, AND 19) AND SIMILAR-TO-ACRP-30 (SEQ ID NO:  
70)

```

SEQ NO 4   MRIWWLLLAIEICTGNINSQDTCRQGHPIPGNPGHNGLPGRDGRDGAAGDKGDAGEPGR
SEQ NO 70   MRIWWLLLAIEICTGNINSQDTCRQGHPIPGNPGHNGLPGRDGRDGAAGDKGDAGEPGR
SEQ NO 10   MRIWWLLLAIEICTGNINSQDTCRQGHPIPGNPGHNGLPGRDGRDGAAGDKGDAGEPGR
SEQ NO 19   MRIWWLLLAIEICTGNINSQDTCRQGHPIPGNPGHNGLPGRDGRDGAAGDKGDAGEPGR
SEQ NO 7     MRIWWLLLAIEICTGNINSQDTCRQGHPIPGNPGHNGLPGRDGRDGAAGDKGDAGEPGR
*****

SEQ NO 4   PGSPGKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGKHGPKGLAGPMGEKGLRGETGP
SEQ NO 70   PGSPGKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGKHGPKGLAGPMGEKGLRGETGP
SEQ NO 10   PGSPGKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGKHGPKGLAGPMGEKGLRGETGP
SEQ NO 19   PGSPGKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGKHGPKGLAGPMGEKGLRGETGP
SEQ NO 7     PGSPGKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGKHGPKGLAGPMGEKGLRGETGP
*****

SEQ NO 4   QGQKGNKGDVGPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGPKGEAGPTGPQ-----
SEQ NO 70   QGQKGNKGDVGPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGPKGEAGPTGPQGEFVVRGI
SEQ NO 10   QGQKGNKGDVGPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGPKGEAGPTGPQGEFVVRGI
SEQ NO 19   QGQKGNKGDVGPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGPKGEAGPTGPQGEFVVRGI
SEQ NO 7     QGQKGNKGDVGPTGPEGPRGNIGPLGPTGLPGPMGPIGKPGPKGEAGPTGPQGEFVVRGI
*****

SEQ NO 4   -----DMPIKFDKILYN-EFNHYDTAAG
SEQ NO 70   RGWKGDRGEKGIKIGETLVLPKSAFTVGLTVLSKFPSSDMPIKFDKILYN-EFNHYDTAAG
SEQ NO 10   RGWKGDRGEKGIKIGETLVLPKSAFTVGLTVLSKFPSSDRPIKFDKILYN-EFNHYDTAAG
SEQ NO 19   RG-----WKGDRGEKGIKIGETLVLPKSAFTVGLTVLS
SEQ NO 7     RG-----WKGDRGEKGIKIGETLVLPKSAFTVGLTVLS
               .  *      : * :  * .  * . .

SEQ NO 4   KFTCHIAGVYYFTYHITVFSRNQVSLVKNQVKILHTKDAYMSSEDQASGGIVLQLKLGD
SEQ NO 70   KFTCHIAGVYYFTYHITVFSRNQVSLVKNQVKILHTKDAYMSSEDQASGGIVLQLKLGD
SEQ NO 10   KFTCHIAGVYYFTYHITVFSRNQVSLVKNQVKILHTKDAYMSSEDQASGGIVLQLKLGD
SEQ NO 19   KFPSSDRPIKFDKIHITVFSRNQVSLVKNQVKILHTKDAYMSSEDQASGGIVLQLKLGD
SEQ NO 7     KFPSSDVPIKFDKIHITVFSRNQVSLVKNQVKILHTRDAYVSSSEDQASGSIVLQLKLGD
**..      : : . *****:***:*****.*****

SEQ NO 4   EVWLQVTGGERFNGLFAEDDDTTFTGFLLFSSP
SEQ NO 70   EVWLQVTGGERFNGLFAEDDDTTFTGFLLFSSP
SEQ NO 10   EVWLQVTGGERFNGLFAEDDDTTFTGFLLFSSP
SEQ NO 19   EVWLQVTGGERFNGLFAEDDDTTFTGFLLFSSP
SEQ NO 7     EMWCVIHRVAKCLSIDP-----FTVASCVRSR
*: *      :      : ..      **      .  *

```

Figure 6

Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES

Applicants: Tianhua Hu  
Docket No.: HYS-46CIP

BLASTP AMINO ACID SEQUENCE ALIGNMENT OF COLLAGEN-LIKE CDCP POLYPEPTIDE (SEQ ID NO: 24) AND HUMAN  $\alpha 1$  TYPE VIII COLLAGEN PRECURSOR (SEQ ID NO: 71)

Score = 1622 bits (4201), Expect = 0.0  
Identities = 742/744 (99%), Positives = 742/744 (99%)

```

SEQ 24: 1   MAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGKPLPPQIPPQMPPQIPQYQPLGQQVPH 60
           MAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGKPLPPQIPPQMPPQIPQYQPLGQQVPH
SEQ 71: 1   MAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGKPLPPQIPPQMPPQIPQYQPLGQQVPH 60

SEQ 24: 61  MPLAKDGLAMGKEMPHLQYGKEYPHLPQYMKEIQAPRMGKEAVPKKGKEIPLASLRGEQ 120
           MPLAKDGLAMGKEMPHLQYGKEYPHLPQYMKEIQAPRMGKEAVPKKGKEIPLASLRGEQ
SEQ 71: 61  MPLAKDGLAMGKEMPHLQYGKEYPHLPQYMKEIQAPRMGKEAVPKKGKEIPLASLRGEQ 120

SEQ 24: 121 GPRGEPGPRGPPGPPGLPGHGIPGIGKPGPGQGYPGVGKPGMPGMPGKPGAMGMPGAKGE 180
           GPRGEPGPRGPPGPPGLPGHGIPGIGKPGPGQGYPGVGKPGMPGMPGKPGAMGMPGAKGE
SEQ 71: 121 GPRGEPGPRGPPGPPGLPGHGIPGIGKPGPGQGYPGVGKPGMPGMPGKPGAMGMPGAKGE 180

SEQ 24: 181 IGQKGEIGPMGIPGPQGPPGPHGLPGIGKPGGPGPLPGQPGPKGDRGPKGLPGPQGLRGPK 240
           IGQKGEIGPMGIPGPQGPPGPHGLPGIGKPGGPGPLPGQPGPKGDRGPKGLPGPQGLRGPK
SEQ 71: 181 IGQKGEIGPMGIPGPQGPPGPHGLPGIGKPGGPGPLPGQPGPKGDRGPKGLPGPQGLRGPK 240

SEQ 24: 241 GDKGFGMPGAPGVKGPPGMHGPPGPVGLPGVGKPGVTGFGPGQGGLGKPGAPGEPGPQGP 300
           GDKGFGMPGAPGVKGPPGMHGPPGPVGLPGVGKPGVTGFGPGQGGLGKPGAPGEPGPQGP
SEQ 71: 241 GDKGFGMPGAPGVKGPPGMHGPPGPVGLPGVGKPGVTGFGPGQGGLGKPGAPGEPGPQGP 300

SEQ 24: 301 IGVPGVQGGPPGIPGIGKPGQDGI PGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPGPKG 360
           IGVPGVQGGPPGIPGIGKPGQDGI PGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPGPKG
SEQ 71: 301 IGVPGVQGGPPGIPGIGKPGQDGI PGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPGPKG 360

SEQ 24: 361 DRGMGGVPGALGPRGEKGPAGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVG 420
           DRGMGGVPGALGPRGEKGPAGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVG
SEQ 71: 361 DRGMGGVPGALGPRGEKGPAGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVG 420

SEQ 24: 421 PQGPPGPKGEPGLQGFPGKPGFLGEVGPPGMRGFGPIGPKGEHGQKGVPLPGVPGLLG 480
           PQGPPGPKGEPGLQGFPGKPGFLGEVGPPGMRG FGPIGPKGE GQKGVPLPGVPGLLG
SEQ 71: 421 PQGPPGPKGEPGLQGFPGKPGFLGEVGPPGMRGLPGPIGPKGEAGQKGVPLPGVPGLLG 480

SEQ 24: 481 PKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFGIGKPGVAGL 540
           PKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFGIGKPGVAGL
SEQ 71: 481 PKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFGIGKPGVAGL 540

SEQ 24: 541 HGPPGKPGALGPQGQPLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHA 600
           HGPPGKPGALGPQGQPLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHA
SEQ 71: 541 HGPPGKPGALGPQGQPLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHA 600

SEQ 24: 601 YGAKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGV 660
           YGAKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGV
SEQ 71: 601 YGAKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGV 660

SEQ 24: 661 YYFAYHVKGGGNVWVAFKNNPEVMYTYDEYKKGFLDQASGSVALLLRPGDRVFLQMPS 720
           YYFAYHVKGGGNVWVAFKNNPEVMYTYDEYKKGFLDQASGSVALLLRPGDRVFLQMPS
SEQ 71: 661 YYFAYHVKGGGNVWVAFKNNPEVMYTYDEYKKGFLDQASGSVALLLRPGDRVFLQMPS 720

SEQ 24: 721 EQAAGLYAGQYVHSSFSGYLLYPM 744
           EQAAGLYAGQYVHSSFSGYLLYPM
SEQ 71: 721 EQAAGLYAGQYVHSSFSGYLLYPM 744

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Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES  
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
8/32

FIGURE 7





BLASTP AMINO ACID SEQUENCE ALIGNMENT OF OTOLIN-LIKE  
CDCP POLYPEPTIDE (SEQ ID NO: 27) AND HUMAN SIMILAR-TO-  
OTOLIN (SEQ ID NO: 78)

```
>gi|37550694|ref|XP_067228.6| similar to otolin-1 [Homo sapiens]
Length = 438

Score = 894 bits (2310), Expect = 0.0
Identities = 434/459 (94%), Positives = 436/459 (94%), Gaps = 21/459 (4%)

SEQ 27: 19  MNTIAKTTPHTKFTKKSEEREMPKGLKPSSGPPPEEEETLFTEMAEMAEPITKPSALDSV 78
              MNTIAKTTPHTKFTKKSEEREMPKGLKPSSGPPPEEEETLFTEMAEMAEPITKPSALDSV
SEQ 78: 1    MNTIAKTTPHTKFTKKSEEREMPKGLKPSSGPPPEEEETLFTEMAEMAEPITKPSALDSV 60

SEQ 27: 79  FGTATLSPFENFTLDPADFFLNCCDCCSPVPGQKGEPGETGQPGPKGEAGNLGIPGPPGV 138
              FGTATLSPFENFTLDPADFFLNCCDCCSPVPGQKGEPGETGQPGPKGEAGNLGIPGPPGV
SEQ 78: 61  FGTATLSPFENFTLDPADFFLNCCDCCSPVPGQKGEPGETGQPGPKGEAGNLGIPGPPGV 120

SEQ 27: 139 VGPQGPGRGYKGEKGLKGERGDQGVPGYPGKPGAQGEPPGPKGDKGNIGLGGVKGQKGSKGD 198
              VGPQ          G +G KGE+G                      EPGPKGDKGNIGLGGVKGQKGSKGD
SEQ 78: 121 VGPQ-----GPRGYKGEKG-----EPGPKGDKGNIGLGGVKGQKGSKGD 159

SEQ 27: 199 TCGNCTKGEKGDQAMGSPGLHGGPGAKGEKGEMGEKGEMGDKGCCGDSGERGGKGQKGE 258
              TCGNCTKGEKGDQAMGSPGLHGGPGAKGEKGEMGEKGEMGDKGCCGDSGERGGKGQKGE
SEQ 78: 160 TCGNCTKGEKGDQAMGSPGLHGGPGAKGEKGEMGEKGEMGDKGCCGDSGERGGKGQKGE 219

SEQ 27: 259 GGMKGEKGSKGDSGMEGKSGRNGLPGAKGDPGIKGEKGELGPPGLLGPTGPKGDIGNKGV 318
              GGMKGEKGSKGDSGMEGKSGRNGLPGAKGDPGIKGEKGELGPPGLLGPTGPKGDIGNKGV
SEQ 78: 220 GGMKGEKGSKGDSGMEGKSGRNGLPGAKGDPGIKGEKGELGPPGLLGPTGPKGDIGNKGV 279

SEQ 27: 319 RGPTGKKGSRGFKGSKGELARVPRSAFSAGLSKPFPPPNIPKFEKILYNDQGNYSPTVG 378
              RGPTGKKGSRGFKGSKGELARVPRSAFSAGLSKPFPPPNIPKFEKILYNDQGNYSPTVG
SEQ 78: 280 RGPTGKKGSRGFKGSKGELARVPRSAFSAGLSKPFPPPNIPKFEKILYNDQGNYSPTVG 339

SEQ 27: 379 KFNC SIPGTYVFSYHITVRGRPARISLVAQNKKQFKSRETLYGQEIDQASLLVILKLSAG 438
              KFNC SIPGTYVFSYHITVRGRPARISLVAQNKKQFKSRETLYGQEIDQASLLVILKLSAG
SEQ 78: 340 KFNC SIPGTYVFSYHITVRGRPARISLVAQNKKQFKSRETLYGQEIDQASLLVILKLSAG 399

SEQ 27: 439 DQVWLEVSKDWNGVYVSAEDDSIFTGFLLYPEETSGISP 477
              DQVWLEVSKDWNGVYVSAEDDSIFTGFLLYPEETSGISP
SEQ 78: 400 DQVWLEVSKDWNGVYVSAEDDSIFTGFLLYPEETSGISP 438
```

FIGURE 9

Title: METHODS AND MATERIALS RELATING TO NOVEL  
Clq DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES  
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
10/32

MULTIPLE AMINO ACID SEQUENCE ALIGNMENT OF GLIACOLIN-LIKE CDCP  
POLYPEPTIDES (SEQ ID NO: 32, 34, 38, AND 41) AND MURINE  
GLIACOLIN (SEQ ID NO: 72)

```

SEQ 32      MVWGRRKSDCDPTMITAFWIGLHLLEGPGQGPVLAANLTILSSKRKVTFFKKQSRGPRPT
SEQ 34      -----
SEQ 72      -----
SEQ 41      -----
SEQ 38      -----
              ::          ::  :  :  :  ::          ::  :  ::          :  :

SEQ 32      FKILSKSRQEDRPALSRLVGSRRRLIAAGALGVMMVLLLVILIPVL-----MLG
SEQ 34      -----MVLLLVILIPVL-----MLG
SEQ 72      -----MVLLLVILIPVLVSSAGTSAHYEMLG
SEQ 41      -----MVLLLLVAIPLLHSSRGPAPHYEMLG
SEQ 38      -----MVLLLLVAIPLLHSSRGPAPHYEMLG
              :  ::          :  ::          ::          :  ::*****:  **:*          ***

SEQ 32      TCRMVCDPYGGTKAPSTAATPDRGLMQSLPTFIQGPKEAGRPGKAGPRGPPGEPGPPGP
SEQ 34      TCRMVCDPYGGTKAPSTAATPDRGLMQSLPTFIQGPKEAGRPGKAGPRGPPGEPGPPGP
SEQ 72      TCRMVCDPYGGTKAPSTAATPDRGLMQSLPTFIQGPKEAGRPGKAGPRGPPGEPGPPGP
SEQ 41      RCRMVCDPHG-PRGPGPDGAP-----ASVPPFPFGAKGEVGRGKAGLRGP---PGPPGP
SEQ 38      RCRMVCDPHG-PRGPGPDGAP-----ASVPPFPFGAKGEVGRGKAGLRGP---PGPPGP
              *****:*  ..*..  :*  :  :  *:*  *  *.****.*  *****  *****

SEQ 32      MGPPGEKGEPGRQGLPGPPGAPGLNAAGAI SAATYSTGPKIAFYAGLRQHEGYEVLKFD
SEQ 34      MGPPGEKGEPGRQGLPGPPGAPGLNAAGAI SAATYSTGPKIAFYAGLRQHEGYEVLKFD
SEQ 72      VGPPGEKGEPGRQGLPGPPGAPGLNAAGAI SAATYSTVPKIAFYAGLRQHEGYEVLKFD
SEQ 41      RGPPGE---PGR---PGPPGPPGPGPGVAPAAGY--VPRIAFYAGLRRPHEGYEVLRF
SEQ 38      RGPPGE---PGR---PGPPGPPGPGPGVAPAAGY--VPRIAFYAGLRRPHEGYEVLRF
              *****  ***  :*****.*  ...*  .**  *  *:*****:*  *****:**

SEQ 32      DVVTNLGNHYDPTTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRASAI AQDA
SEQ 34      DVVTNLGNHYDPTTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRASAI AQDA
SEQ 72      DVVTNLGNHYDPTTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRASAI AQDA
SEQ 41      DVVTNVGNAYEAA SGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAI AQDA
SEQ 38      DVVTNVGNAYEAA SGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQGWGPRTALPS
              *****:*  *:  :  :  *****:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

SEQ 32      DQNYDYASNS-----VVLHLE-----PGDEVYIKLD-GGKAHGG
SEQ 34      DQNYDYASNS-----VVLHLE-----PGDEVYIKLD-GGKAHGG
SEQ 72      DQNYDYASNS-----VVLHLE-----PGDEVYIKLD-GGKAHGG
SEQ 41      DQNYDYASNS-----VILHLD-----VGDEVFIKLD-GGKVHGG
SEQ 38      AESVAWQLKGQPGASAIICLLRVTVIQWESLVVPPFSTYGCQPQEDDGLRFCSGASPVAG
              :.  :  :.          :  :  :  :          :  :  :  :  *..  .*

SEQ 32      NNN-----KYSTF--SGFIIYAD-----
SEQ 34      NNN-----KYSTF--SGFIIYAD-----
SEQ 72      NNN-----KYSTF--SGFIIYAD-----
SEQ 41      NTN-----KYSTF--SGFIIYPD-----
SEQ 38      NCNPQDDARAQLPSFYVAEFMLPCTEQTLSTQPCPSPCPVIE
              *  *          :  :  *  :  *  :

```

FIGURE 10

Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES  
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
11/32

MULTIPLE AMINO ACID SEQUENCE ALIGNMENT OF GLIACOLIN-LIKE CDCP  
POLYPEPTIDES (SEQ ID NO: 32, 34, 38, AND 41) AND HUMAN CRF (SEQ  
ID NO: 73)

```

SEQ 32      MVWGRRKSDQCDPTMITAFWIGLHLLEGPGVPLAANLTILSSKRKVTFFKKQSRRGPRPT
SEQ 34      -----
SEQ 73      -----
SEQ 41      -----
SEQ 38      -----
              ::          ::  : : : ::          ::  : ::          : :

SEQ 32      FKILSKSRQEDRPALSRLVGSRRRLIAAGALGVVMVLLLVILIPVL-----MLG
SEQ 34      -----MVLVVILIPVL-----MLG
SEQ 73      -----MLLVVLIPVLVSSGGPEGHYEMLG
SEQ 41      -----MVLVVVAIPLLHSSRGPAPHYEMLG
SEQ 38      -----MVLVVVAIPLLHSSRGPAPHYEMLG
              : ::          :  ::          ::          : ::*:*:*:*:  **:*          ***

SEQ 32      TCRMVCDPYGGTKAPSTAATPDRGLMQS-----LPTFIQGPKEAGRPGKAGPRGPPG
SEQ 34      TCRMVCDPYGGTKAPSTAATPDRGLMQS-----LPTFIQGPKEAGRPGKAGPRGPPG
SEQ 73      TCRMVCDPYP-ARGPGAGARTDGGDALSEQSGAPPSTLVQGPQKPGRTGKPGPPGPPG
SEQ 41      RCRMVCDPHG-PRGPGPDGAPAS-----VPPFPFGAKGEVGRRGKAGLRGPPG
SEQ 38      RCRMVCDPHG-PRGPGPDGAPAS-----VPPFPFGAKGEVGRRGKAGLRGPPG
              *****:  .:.*. . . . .          . . :  *.:*:  **  **.*  ****

SEQ 32      EPGPPGPMGPPGEKGEPRQGLPGPPGAPGLNAAGAI SAATYSTGPKIAFYAGLRQHEG
SEQ 34      EPGPPGPMGPPGEKGEPRQGLPGPPGAPGLNAAGAI SAATYSTGPKIAFYAGLRQHEG
SEQ 73      DPGPPGPMGPPGEKGEKPGK---PGPPGLPGAGGSGAISTATYTTVPRVAFYAGLRNPHEG
SEQ 41      ---PPGPRGPPGE---PGR---PGPPGPPGPGPGGVAPAAGY--VPRIAFYAGLRNPHEG
SEQ 38      ---PPGPRGPPGE---PGR---PGPPGPPGPGPGGVAPAAGY--VPRIAFYAGLRNPHEG
              ****  *****  **:  :*****  **  .  .*.  .: *  *  *:*****:  ****

SEQ 32      YEVLKFDDVVTNLGNHYDPTTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRA
SEQ 34      YEVLKFDDVVTNLGNHYDPTTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRA
SEQ 73      YEVLKFDDVVTNLGNHYDAASGKFTCNIPGIYFFTYHVLMRGGDGTSMWADLCKNGQVRA
SEQ 41      YEVLRFDDVVTNNGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRA
SEQ 38      YEVLRFDDVVTNNGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQGWG
              ****:*****: **  *: .: :*****  : **  ***:*****  ****  *  .

SEQ 32      SAIAQDADQNYDYASN-----SVVLHLE-----PGDEVYIKLD
SEQ 34      SAIAQDADQNYDYASN-----SVVLHLE-----PGDEVYIKLD
SEQ 73      SAIAQDADQNYDYASN-----SVILHLD-----AGDEVFIKLD
SEQ 41      SAIAQDADQNYDYASN-----SVILHLD-----VGDEVFIKLD
SEQ 38      PRTALPSAESVAWQLKGQPGASAIICLLRVTVIQWESLVPPFSTYCGPQEDDGLRFCS
              .  *  :  :  :  :  *.: :  *          *:  .

SEQ 32      GGKAHGGNNN-----KYSTF--SGFIIYAD-----
SEQ 34      GGKAHGGNNN-----KYSTF--SGFIIYAD-----
SEQ 73      GGKAHGGNSN-----KYSTF--SGFIIYSD-----
SEQ 41      GGKVHGGNTN-----KYSTF--SGFIIYPD-----
SEQ 38      GASPVAGNCNPQDDARAQLPSFYVAEFMLPCTEQTLSTQPCSPSPCVIPE
              *..  .**  *          :  :.*  :  *:

```

FIGURE 11

Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES  
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
12/32

MULTIPLE AMINO ACID SEQUENCE ALIGNMENT OF GLIACOLIN-LIKE CDCP  
POLYPEPTIDES (SEQ ID NO: 46, 48, AND 51) AND HUMAN EEG1L (SEQ ID  
NO: 74)

```

SEQ 46      -----
SEQ 51      -----
SEQ 48      -----
SEQ 74      MEVQVSQASLGFELTSVEKSLREWSRLSREVIAWLCPSSPNFILNFPPPPSASSVSMVQL

SEQ 46      -----
SEQ 51      -----MKSAPQVNHSQHGESQRALSPLQSTLSSAASPSQAYET
SEQ 48      -----
SEQ 74      FSSPFGYQSPSGHSEEEREGNMKSAPQVNHSQHGESQRALSPLQSTLSSAASPSQAYET

SEQ 46      -----
SEQ 51      YIENGLICLKHKIRNIEKKKLKLEDYKDRLKSGEHLNPDQLEAVEKYEEVLHNLEFAKEL
SEQ 48      -----
SEQ 74      YIENGLICLKHKIRNIEKKKLKLEDYKDRLKSGEHLNPDQLEAVEKYEEVLHNLEFAKEL

SEQ 46      -----
SEQ 51      QKTFSGLSLDLLKAQKKAQRREHMLKLEAEKKKLRTILQVQYVLQNLQEHVQKDFKGGL
SEQ 48      -----
SEQ 74      QKTFSGLSLDLLKAQKKAQRREHMLKLEAEKKKLRTILQVQYVLQNLQEHVQKDFKGGL

SEQ 46      -----
SEQ 51      NGAVYLPSKELDYLKFSKLTCPERNESLSVEDQMEQSSLYFWDLLEGSEKAVVGTTYKH
SEQ 48      -----
SEQ 74      NGAVYLPSKELDYLKFSKLTCPERNESLSVEDQMEQSSLYFWDLLEGSEKAVVGTTYKH

SEQ 46      -----MLIQSEKKTQLSKTESVKESESLMEFA
SEQ 51      LKDLLSKLLNSGYFESIPVPKNAKEKEVPLEEMLIQSEKKTQLSKTESVKESESLMEFA
SEQ 48      -----MLIQSEKKTQLSKTESVKESESLMEFA
SEQ 74      LKDLLSKLLNSGYFESIPVPKNAKEKEVPLEEMLIQSEKKTQLSKTESVKESESLMEFA
                      *****

SEQ 46      QPEIQPQEFLNRRYMTEVDYSNKQGEEQPWEADYARKPNLPKRWDMLTEPDGQEKKQESF
SEQ 51      QPEIQPQEFLNRRYMTEVDYSNKQGEEQPWEADYARKPNLPKRWDMLTEPDGQEKKQESF
SEQ 48      QPEIQPQEFLNRRYMTEVDYSNKQGEEQPWEADYARKPNLPKRWDMLTEPDGQEKKQESF
SEQ 74      QPEIQPQEFLNRRYMTEVDYSNKQGEEQPWEADYARKPNLPKRWDMLTEPDGQEKKQESF
                      *****

SEQ 46      KSWEASGKHQEVSKPAVSLEQRKQDTSKLRSTLPEEQKKQEISKSKSPSPSQWKQDTPKSK
SEQ 51      KSWEASGKHQEVSKPAVSLEQRKQDTSKLRSTLPEEQKKQEISKSKSPSPSQWKQDTPKSK
SEQ 48      KSWEASGKHQEVSKPAVSLEQRKQDTSKLRSTLPEEQKKQEISKSKSPSPSQWKQDTPKSK
SEQ 74      KSWEASGKHQEVSKPAVSLEQRKQDTSKLRSTLPEEQKKQEISKSKSPSPSQWKQDTPKSK
                      *****

SEQ 46      AGYVQEEQKKQETPKLWPVQLQKEQDPKKQTPKSWTPSMQSEQNTTKSWTTPMCEEQDSK
SEQ 51      AGYVQEEQKKQETPKLWPVQLQKEQDPKKQTPKSWTPSMQSEQNTTKSWTTPMCEEQDSK
SEQ 48      AGYVQEEQKKQETPKLWPVQLQKEQDPKKQTPKSWTPSMQSEQNTTKSWTTPMCEEQDSK
SEQ 74      AGYVQEEQKKQETPKLWPVQLQKEQDPKKQTPKSWTPSMQSEQNTTKSWTTPMCEEQDSK
                      *****

```

```

SEQ 46      QPETPKSWENNVESQKHSLSQSQISPKSWG VATASLI PNDQLLPRKLNTEPKDVPKPVH
SEQ 51      QPETPKSWENNVESQKHSLSQSQISPKSWG VATASLI PNDQLLPRKLNTEPKDVPKPVH
SEQ 48      QPETPKSWENNVESQKHSLSQSQISPKSWG VATASLI PNDQLLPRKLNTEPKDVPKPVH
SEQ 74      QPETPKSWENNVESQKHSLSQSQISPKSWG VATASLI PNDQLLPRKLNTEPKDVPKPVH
*****

SEQ 46      QPVGSSSTL PKDPVLRKEKLQDLMTQIQGTCNFMQESVLDFDKPSSA IPTSQPPSATPGS
SEQ 51      QPVGSSSTL PKDPVLRKEKLQDLMTQIQGTCNFMQESVLDFDKPSSA IPTSQPPSATPGS
SEQ 48      QPVGSSSTL PKDPVLRKEKLQDLMTQIQGTCNFMQESVLDFDKPSSA IPTSQPPSATPGS
SEQ 74      QPVGSSSTL PKDPVLRKEKLQDLMTQIQGTCNFMQESVLDFDKPSSA IPTSQPPSATPGS
*****

SEQ 46      PVASKEQNLSSQSDFLQEPLQATSSPVTCSSNACLVT TDQASSGSETEFMTSETPEAAIP
SEQ 51      PVASKEQNLSSQSDFLQEPLQATSSPVTCSSNACLVT TDQASSGSETEFMTSETPEAAIP
SEQ 48      PVASKEQNLSSQSDFLQEPLQ-----
SEQ 74      PVASKEQNLSSQSDFLQEPLQATSSPVTCSSNACLVT TDQASSGSETEFMTSETPE----
*****
:           :           :           :           :

SEQ 46      PGKQPSSLASPNPPMAKGSEQGFQSPPASSSSVTINTAPFQAMQTVFNVNAPLPPRKEQE
SEQ 51      PGKQPSSLASPNPPMAKGSEQGFQSPPASSSSVTINTAPFQAMQTVFNVNAPLPPRKEQE
SEQ 48      -----VFNVNAPLPPRKEQE
SEQ 74      -----VFNVNAPLPPRKEQE
:           :           :           :           : *****

SEQ 46      IKESPYSPGYNQSF TTA STQTTPQCQLPSIHVEQTVHSQETAN-YHPDGTIQVSNGLAF
SEQ 51      IKESPYSPGYNQSF TTA STQTTPQCQLPSIHVEQTVHSQETAN-YHPDGTIQVSNGLAF
SEQ 48      IKESPYSPGYNQSF TTA STQTTPQCQLPSIHVEQTVHSQETAANYHPDGTIQVSNGLAF
SEQ 74      IKESPYSPGYNQSF TTA STQTTPQCQLPSIHVEQTVHSQETAN-YHPDGTIQVSNGLAF
*****

SEQ 46      YPAQTNVFP RPTQPFVNSRGSVRGCTRGRLITNSYRSPGGYKGFDTYRGLPSISNGNYS
SEQ 51      YPAQTNVFP RPTQPFVNSRGSVRGCTRGRLITNSYRSPGGYKGFDTYRGLPSISNGNYS
SEQ 48      YPAQTNVFP RPTQPFVNSRGSVRGCTRGRLITNSYRSPGGYKGFDTYRGLPSISNGNYS
SEQ 74      YPAQTNVFP RPTQPFVNSRGSVRGCTRGRLITNSYRSPGGYKGFDTYRGLPSISNGNYS
*****

SEQ 46      QLQFQAREYSGAPYSQR--CLETSEPLWLLGKARI ISSSVISEEGLV VHEQIREVSSPE
SEQ 51      QLQFQAREYSGAPYSQRDNFQQCYKRGGTSGGPRANSRAGWSDS-----SQVSSPE
SEQ 48      QLQFQAREYSGAPYSQRDNFQQCYKRGGTSGGPRANSRAGWSDS-----SQVSSPE
SEQ 74      QLQFQAREYSGAPYSQRDNFQQCYKRGGTSGGPRANSRAGWSDS-----SQVSSPE
*****
:           :           * . * : * : . : : : : *****

SEQ 46      RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYPLPQQMRVAFSAARTSNLAPG
SEQ 51      RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYPLPQQMRVAFSAARTSNLAPG
SEQ 48      RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYPLPQQMRVAFSAARTSNLAPG
SEQ 74      RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYPLPQQMRVAFSAARTSNLAPG
*****

SEQ 46      TLDQPIVFDLLLNNLGETFDLQLGRFNC PVNGTYVFI FHMLKLAVNVPLYVNL MKNEEVL
SEQ 51      TLDQPIVFDLLLNNLGETFDLQLGRFNC PVNGTYVFI FHMLKLAVNVPLYVNL MKNEEVL
SEQ 48      TLDQPYGVDLLLNNLGETFDLQLGRFNC PVNGTYVFI FHMLKLAVNVPLYVNL MKNEEVL
SEQ 74      TLDQPIVFDLLLNNLGETFDLQLGRFNC PVNGTYVFI FHMLKLAVNVPLYVNL MKNEEVL
*****

SEQ 46      VSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYLLYQD
SEQ 51      VSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYLLYQD
SEQ 48      VSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYLLYQD
SEQ 74      VSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYLLYQD

```

FIGURE 12B

Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES

Applicants: Tianhua Hu  
Docket No.: HYS-46CIP

BLASTP AMINO ACID SEQUENCE ALIGNMENT OF EMILIN-LIKE  
CDCP POLYPEPTIDE (SEQ ID NO: 55) AND HUMAN EMILIN-2  
PRECURSOR (SEQ ID NO: 77)

```
>gi|14042988| extracellular glycoprotein EMILIN-2 precursor [Homo sapiens]
Length = 1053

Score = 547 bits (1410), Expect = e-154
Identities = 264/267 (98%), Positives = 265/267 (98%)

SEQ 55: 247 EAPSPPPPAEAPKEPLQPEPAPPRPSGPATAEDPGRRPVLPQRPPEERPPQPPGSTGVIA 306
      +APSPPPPAEAPKEPLQPEPAPPRPSGPATAEDPGRRPVLPQRPPEERPPQPPGSTGVIA
SEQ 77: 787 KAPSPPPPAEAPKEPLQPEPAPPRPSGPATAEDPGRRPVLPQRPPEERPPQPPGSTGVIA 846

SEQ 55: 307 ETGQAGPPAGAGVSGRGLPRGVDGQTGSGTVPGAEGFAGAPGYPKSPPVASPGAPVPSLV 366
      ETGQAGPPAGAGVSGRGLPRGVDGQTGSGTVPGAEGFAGAPGYPKSPPVASPGAPV SLV
SEQ 77: 847 ETGQAGPPAGAGVSGRGLPRGVDGQTGSGTVPGAEGFAGAPGYPKSPPVASPGAPVSSLV 906

SEQ 55: 367 SFSAGLTQKPFPSDGGVVLFNKVLVNDGDVYNPSTGVFTAPYDGRYLITATLTPERDAYV 426
      SFSAGLTQKPFPSDGGVVLFNKVLVNDGDVYNPSTGVFTAPYDGRYLITATLTPERDAYV
SEQ 77: 907 SFSAGLTQKPFPSDGGVVLFNKVLVNDGDVYNPSTGVFTAPYDGRYLITATLTPERDAYV 966

SEQ 55: 427 EAVLSVSNASVAQLHTAGYRREFLEYHRPTGALHTCGGPGAFHLIVHLKAGDAVNVVVTG 486
      EAVLSVSNASVAQLHTAGYRREFLEYHRP GALHTCGGPGAFHLIVHLKAGDAVNVVVTG
SEQ 77: 967 EAVLSVSNASVAQLHTAGYRREFLEYHRPPGALHTCGGPGAFHLIVHLKAGDAVNVVVTG 1026

SEQ 55: 487 GKLAHTDFDEMYSTFSGVFLYPFLSHL 513
      GKLAHTDFDEMYSTFSGVFLYPFLSHL
SEQ 77: 1027 GKLAHTDFDEMYSTFSGVFLYPFLSHL 1053
```

FIGURE 13

BLASTP AMINO ACID SEQUENCE ALIGNMENT OF C1QTNF-LIKE  
CDCP POLYPEPTIDE (SEQ ID NO: 59) AND HUMAN C1QTNF7 (SEQ  
ID NO: 75)

>gi|13994280| C1q and tumor necrosis factor related protein 7; [Homo sapiens]  
Length = 289

Score = 611 bits (1576), Expect = e-174  
Identities = 289/289 (100%), Positives = 289/289 (100%)

```

SEQ 59: 1   MFVLLYVTSFAICASGQPRGNQLKGENYSPRYICSIPGLPGPPGPPGANGSPGPHGRIGL 60
           MFVLLYVTSFAICASGQPRGNQLKGENYSPRYICSIPGLPGPPGPPGANGSPGPHGRIGL
SEQ 75: 1   MFVLLYVTSFAICASGQPRGNQLKGENYSPRYICSIPGLPGPPGPPGANGSPGPHGRIGL 60

SEQ 59: 61   PGRDGRDGRKGEKGEKGTAGLRGKTGPLGLAGEKGDQGETGKKGPIGPEGEKGEVGPIGP 120
           PGRDGRDGRKGEKGEKGTAGLRGKTGPLGLAGEKGDQGETGKKGPIGPEGEKGEVGPIGP
SEQ 75: 61   PGRDGRDGRKGEKGEKGTAGLRGKTGPLGLAGEKGDQGETGKKGPIGPEGEKGEVGPIGP 120

SEQ 59: 121  PGPKGDRGEQGDPLPGVCRCGSIVLKSAFSVGITTSYPEERLPIIFNKVLFNEGEHYNP 180
           PGPKGDRGEQGDPLPGVCRCGSIVLKSAFSVGITTSYPEERLPIIFNKVLFNEGEHYNP
SEQ 75: 121  PGPKGDRGEQGDPLPGVCRCGSIVLKSAFSVGITTSYPEERLPIIFNKVLFNEGEHYNP 180

SEQ 59: 181  ATGKFICAFPGIYYFSYDITLANKHLAIGLVHNGQYRIKTFDANTGNHDTVASGSTVIYLQ 240
           ATGKFICAFPGIYYFSYDITLANKHLAIGLVHNGQYRIKTFDANTGNHDTVASGSTVIYLQ
SEQ 75: 181  ATGKFICAFPGIYYFSYDITLANKHLAIGLVHNGQYRIKTFDANTGNHDTVASGSTVIYLQ 240

SEQ 59: 241  PEDEVWLEIFFTDQNGLFSDPGWADSLFSGFLLYVDTDYLDSISEDDEL 289
           PEDEVWLEIFFTDQNGLFSDPGWADSLFSGFLLYVDTDYLDSISEDDEL
SEQ 75: 241  PEDEVWLEIFFTDQNGLFSDPGWADSLFSGFLLYVDTDYLDSISEDDEL 289

```

FIGURE 14



BLASTP AMINO ACID SEQUENCE ALIGNMENT OF C1QTNF-LIKE  
CDCP POLYPEPTIDE (SEQ ID NO: 63) AND HUMAN C1QTNF6 (SEQ  
ID NO: 76)

>gi|32967294|C1q and tumor necrosis factor related protein 6 [Homo sapiens]  
Length = 278

Score = 538 bits (1387), Expect = e-152  
Identities = 259/259 (100%), Positives = 259/259 (100%)

```

SEQ 63: 1  MGTAALGPVWAALLLFLLMCEIPMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGR 60
           MGTAALGPVWAALLLFLLMCEIPMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGR
SEQ 76: 20  MGTAALGPVWAALLLFLLMCEIPMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGR 79

SEQ 63: 61  PHALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKDKGEMGSPGAPC 120
           PHALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKDKGEMGSPGAPC
SEQ 76: 80  PHALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKDKGEMGSPGAPC 139

SEQ 63: 121 QKRFFAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHS 180
           QKRFFAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHS
SEQ 76: 140 QKRFFAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHS 199

SEQ 63: 181 WNYKETYVHIMHNQKEAVILYAQP SERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYS 240
           WNYKETYVHIMHNQKEAVILYAQP SERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYS
SEQ 76: 200 WNYKETYVHIMHNQKEAVILYAQP SERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYS 259

SEQ 63: 241 NDFDTYITFSGHLIKAEDD 259
           NDFDTYITFSGHLIKAEDD
SEQ 76: 260 NDFDTYITFSGHLIKAEDD 278

```

FIGURE 15

# ALIGN0 NUCLEIC ACID SEQUENCE ALIGNMENT OF C1QTNF-LIKE CDCP POLYNUCLEOTIDES (SEQ ID NO: 62 AND 65)

SEQ ID NO: 62 (2944 nt) vs. SEQ ID NO: 65 (1651 nt)  
scoring matrix: DNA, gap penalties: -16/-4  
41.7% identity; Global alignment score: 3732

```

      10      20      30      40      50
SEQ 62 GCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGAAAGCTA-----AGT
      : : : : : : : : : : : : : : : : : :
SEQ 65 -----TGGGCCTGGGGGTCTGGGCCAGCAACAAGTTAGT
      10      20      30

      60      70      80      90      100
SEQ 62 CTTCCCTTTATCGAGTCAAGAAACCCC--CCCTTCTTGAGCTATT--TACAGCTTTTAA
      : : : : : : : : : : : : : : : : : :
SEQ 65 ATTGCCAGACAT-GGGCCAAGGAGCCAGAGGCCATGCAGTGGCTCAGGGTCCGTGAGTCGC
      40      50      60      70      80      90

      110      120      130      140      150      160
SEQ 62 CAATTGAGT--AAAGTACGCTCCGGTCACCATGGGGACAGCCGCCCTGGGTCCCGTCTGG
      : : : : : : : : : : : : : : : : : :
SEQ 65 CTGGGGAGGCCACAGGACACAG-GGTCACCATGGGGACAGCCGCCCTGGGTCCCGTCTGG
      100      110      120      130      140      150

      170      180      190      200      210      220
SEQ 62 GCAGCGCTCCTGCTCTTTCTCCTGATGTGTGAGATCCCTATGGTGGAGCTCACCTTTGAC
      : : : : : : : : : : : : : : : : : :
SEQ 65 GCAGCGCTCCTGCTCTTTCTCCTGATGTGTGAGATCCCTATGGTGGAGCTCACCTTTGAC
      160      170      180      190      200      210

      230      240      250      260      270      280
SEQ 62 AGAGCTGTGGCCAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCC
      : : : : : : : : : : : : : : : : : :
SEQ 65 AGAGCTGTGGCCAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCC
      220      230      240      250      260      270

      290      300      310      320      330      340
SEQ 62 CATGTATCCTCAGCCTCTTCCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTAC
      : : : : : : : : : : : : : : : : : :
SEQ 65 CATGTATCCTCAGCCTCTTCCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTAC
      280      290      300      310      320      330

      350      360      370      380      390      400
SEQ 62 ATTAATATCACCATCCTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGG
      : : : : : : : : : : : : : : : : : :
SEQ 65 ATTAATATCACCATCCTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGG
      340      350      360      370      380      390

      410      420      430      440      450      460
SEQ 62 TACATGGGCAGGGAGGGTCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAG
      : : : : : : : : : : : : : : : : : :
SEQ 65 TACATGGGCAGGGAGGGTCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAG
      400      410      420      430      440      450

```

FIGURE 16A

Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES  
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
18/32



```

1010      1020      1030      1040      1050      1060
SEQ 62 CCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGACCCTGCTTCTATCTTGGCTGCCA
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 -CTGGGA--TCCCCCTT--CCTGCC-TCCTCCCAGGGCTCTGCCAGGGCCTTG-CT--CA
      980          990          1000          1010          1020

1070      1080      1090      1100      1110      1120
SEQ 62 TCATCCCTCCCAGCCTATT--TCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAGAAGC
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 --GTCCCTTCCACCAAAGTCATCTGAAC TTC-CGTTTCCCCAGGGCCT-----C
      1030          1040          1050          1060          1070

1130      1140      1150      1160      1170      1180
SEQ 62 TTGCTAACCTAA-ATATTCTAGAACTTTCCCAGC--CTCGTAGCCCAGCA--CTTCTCAA
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 CAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCTCTCTGCCCTCATGCCCTCTC
      1080          1090          1100          1110          1120          1130

1190      1200      1210      1220      1230      1240
SEQ 62 ACTTGGAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCTGACTCAGCAG
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 ACCGGCCCAGTGCCCCGACTCTCCAGGCTTT-----ATCAAGGTGCTAAG---GCCC
      1140          1150          1160          1170          1180

1250      1260      1270      1280      1290      1300
SEQ 62 GTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCCCTGGGTGATGCTGATGGGGTC
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 GGGTGGGCAGCTCCTCGTCTCAGAGCC-CTCCTCCGG-CCTGG-TGCTGCCTTTACAAAC
      1190          1200          1210          1220          1230

1310      1320      1330      1340      1350
SEQ 62 AGTCTATGAACCA----CACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTA
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 ACCTGCAGGAGAAGGGCCACGGAAGCC-CCAGGCTTTAGAGCCCTCAGCAGGTCTGGGGA
      1240          1250          1260          1270          1280          1290

1360      1370      1380      1390      1400      1410
SEQ 62 CTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCT
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 GCTAGAGCAAAGGAGGGA--CCTCAGGCCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCCT
      1300          1310          1320          1330          1340          1350

1420      1430      1440      1450      1460      1470
SEQ 62 TGAGA---CAGAGTCTTGCTCTGTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTC
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 GGTGTTCCCCTAGCCTTCCA----AATCCAGG-TGGCCTGCCCTTCTCC----CCAGAGG
      1360          1370          1380          1390          1400

1480      1490      1500      1510      1520      1530
SEQ 62 ACTGCAACCTCTGCCTCCCGG-GTTCAAGC-GATTCTTCTGCCTCAGCCTCCCTAGTGGC
      : : : : : : : : : : : : : : : : : : : :
SEQ 65 GAGGCGGCCCTCCGCCCATTTGGTGCTCATGCAGACTCTGGGGC-TGAGGTGCCCCGGGGGG
      1410          1420          1430          1440          1450          1460

```

FIGURE 16C

```

      1540      1550      1560      1570      1580
SEQ 62 TGGGATTACAGGCGCCTGCTACCATG----CCTGGCTAATTTTTGTATTTTAGTAGAGA
      :: :: : :: :: : :: : : :: :: : : :: :: : : :: :
SEQ 65 TG--ATCTCTGGTGCACAGCCGAGGAGCCGTGGCTCC---ATGGCCAGATGACGGAAA
      1470      1480      1490      1500      1510

      1590      1600      1610      1620      1630
SEQ 62 TGGGGTTTCACCATATTGGCCAGG-----CTGGTCT-TGAACT--CCTGACTTCAGGTGA
      :: :: : :: :: : :: :: : :: :: : :: :: : :: :: :
SEQ 65 CAGGGTCTGACCAAGT--GCCAGGAAGACCTGTGCTATAAACCACCCTGCCTGATCCTGC
      1520      1530      1540      1550      1560      1570

      1640      1650      1660      1670      1680      1690
SEQ 62 CCCA-----CCCGCCTCGGCCCTCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTG
      :: :: :: :: :: : :: :: : :: :: : :: :: : :: :: :
SEQ 65 CCCTGCCCTGACCCCGCCACGCCCTGCCGTCCAGCATG-ATTAAAGAATGCTGTCTCCT--
      1580      1590      1600      1610      1620      1630

      1700      1710      1720      1730      1740      1750
SEQ 62 CCTGGCCAATTCCAACATTCTTAAATTCTCTCATCCCTCCAGGGCTCCCCGTGCTATGTT
      : :: :: : :: :
SEQ 65 CTTGGCAAAAAAAAAA-----
      1640      1650

      1760      1770      1780      1790      1800      1810
SEQ 62 CTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGCCTGCACCACCTGCAGCCACCGTTCAT
SEQ 65 -----

      1820      1830      1840      1850      1860      1870
SEQ 62 TTATTCATTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGG
SEQ 65 -----

      1880      1890      1900      1910      1920      1930
SEQ 62 GTCAGACACAGGCCCTGCCCCTGCCCTCAGTGACTGGCCAGTCCAGCCCAGGCGGGGAGA
SEQ 65 -----

      1940      1950      1960      1970      1980      1990
SEQ 62 GATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGGGCCTGTGTTCTGGGTGTT
SEQ 65 -----

      2000      2010      2020      2030      2040      2050
SEQ 62 CAGGTGCTGCTGGTCCCTCCATTACCCACTGCTCCCCAAGGCTGGTGGGACGGGGTCCCGG
SEQ 65 -----

```

FIGURE 16D

	2060	2070	2080	2090	2100	2110
SEQ 62	TGGCAGGGGCAGGTATCTCCTTCCCCGTTCCCTCATCCACCTGCCCAGTGCTCATCGTTACA					
SEQ 65	-----					
	2120	2130	2140	2150	2160	2170
SEQ 62	GCAAACCCCAGGGGGCCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGGACCCAGGAGTGT					
SEQ 65	-----					
	2180	2190	2200	2210	2220	2230
SEQ 62	GGGGGCATTTGGGGGGTGAAGTGGCCCCCGAAGAATGGAACCCACACCCATAGCTCTCCC					
SEQ 65	-----					
	2240	2250	2260	2270	2280	2290
SEQ 62	CACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCCCCTTCTCTGC					
SEQ 65	-----					
	2300	2310	2320	2330	2340	2350
SEQ 62	CTCCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCATCTGAACTT					
SEQ 65	-----					
	2360	2370	2380	2390	2400	2410
SEQ 62	CCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCTCTCT					
SEQ 65	-----					
	2420	2430	2440	2450	2460	2470
SEQ 62	GCCCCTCATGCCCCCTCTACCGGGCCAGTGCCCCGACTCTCCAGGC'TTTATCAAGGTGCT					
SEQ 65	-----					
	2480	2490	2500	2510	2520	2530
SEQ 62	AAGGCCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTCCGGCCTGGTGCTGCCTTTAC					
SEQ 65	-----					
	2540	2550	2560	2570	2580	2590
SEQ 62	AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGG					
SEQ 65	-----					

FIGURE 16E

Title: METHODS AND MATERIALS RELATING TO NOVEL  
 Clq DOMAIN-CONTAINING POLYPEPTIDES AND  
 POLYNUCLEOTIDES  
 Applicants: Tianhua Hu  
 Docket No.: HYS-46CIP  
 22/32

	2600	2610	2620	2630	2640	2650
SEQ 62	GGAGCTAGAGCAAAGGAGGGACCTCAGGCCTCCGTTTCTTCTTCCAGGGTGGGGTGGCC					
SEQ 65	-----					
	2660	2670	2680	2690	2700	2710
SEQ 62	TGGTGTTCCTCCCTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGCGGC					
SEQ 65	-----					
	2720	2730	2740	2750	2760	2770
SEQ 62	CTCCGCCCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCCGGGGGTGATCTCTG					
SEQ 65	-----					
	2780	2790	2800	2810	2820	2830
SEQ 62	GTGCTCACAGCCGAGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAA					
SEQ 65	-----					
	2840	2850	2860	2870	2880	2890
SEQ 62	GTGCCAGGAAGACCTGTGCTATAAACCACCTGCCTGATCCTGCCCTGCCTGACCCCGC					
SEQ 65	-----					
	2900	2910	2920	2930	2940	
SEQ 62	CACGCCCTGCCGTCCAGCATGATTAAAGAATGCTGTCTCCTCAAAAAAAAAA					
SEQ 65	-----					

FIGURE 16F

# ALIGN0 NUCLEIC ACID SEQUENCE ALIGNMENT OF C1QTNF-LIKE CDCP POLYNUCLEOTIDES (SEQ ID NO: 62 AND 66)

SEQ ID NO: 62 (2944 nt) vs. SEQ ID NO: 66 (2929 nt)  
scoring matrix: DNA, gap penalties: -16/-4  
96.8% identity; Global alignment score: 13971

```

      10      20      30      40      50
SEQ 62 GCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGAAAGCTA-----AGT
      : : : : : : : : : : : : : : : : : :
SEQ 66 -----TGGGCCTGGGGGTCTGGGCCAGCAACAAGTTAGT
      10      20      30

      60      70      80      90      100
SEQ 62 CTTCCCTTTATCGAGTCAAGAAACCCC---CCCTTCTTGAGCTATT--TACAGCTTTTAA
      : : : : : : : : : : : : : : : : : :
SEQ 66 ATTCAGACAT-GGGCCAAGGAGCCAGAGGCCATGCAGTGGCTCAGGGTCCGTGAGTCGC
      40      50      60      70      80      90

      110      120      130      140      150      160
SEQ 62 CAATTGAGT--AAAGTACGCTCCGGTCACCATGGGGACAGCCGCCCTGGGTCCCGTCTGG
      : : : : : : : : : : : : : : : : : :
SEQ 66 CTGGGGAGGCCACAGGACACAG-GGTCACCATGGGGACAGCCGCCCTGGGTCCCGTCTGG
      100      110      120      130      140      150

      170      180      190      200      210      220
SEQ 62 GCAGCGCTCCTGCTCTTTCTCCTGATGTGTGAGATCCCTATGGTGGAGCTCACCTTTGAC
      : : : : : : : : : : : : : : : : : :
SEQ 66 GCAGCGCTCCTGCTCTTTCTCCTGATGTGTGAGATCCCTATGGTGGAGCTCACCTTTGAC
      160      170      180      190      200      210

      230      240      250      260      270      280
SEQ 62 AGAGCTGTGGCCAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCC
      : : : : : : : : : : : : : : : : : :
SEQ 66 AGAGCTGTGGCCAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCC
      220      230      240      250      260      270

      290      300      310      320      330      340
SEQ 62 CATGTATCCTCAGCCTCTTCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTAC
      : : : : : : : : : : : : : : : : : :
SEQ 66 CATGTATCCTCAGCCTCTTCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTAC
      280      290      300      310      320      330

      350      360      370      380      390      400
SEQ 62 ATTAATATCACCATCCTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGG
      : : : : : : : : : : : : : : : : : :
SEQ 66 ATTAATATCACCATCCTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGG
      340      350      360      370      380      390

      410      420      430      440      450      460
SEQ 62 TACATGGGCAGGGAGGGTCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAG
      : : : : : : : : : : : : : : : : : :
SEQ 66 TACATGGGCAGGGAGGGTCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAG
      400      410      420      430      440      450

```

FIGURE 17A

Title: METHODS AND MATERIALS RELATING TO NOVEL  
C1q DOMAIN-CONTAINING POLYPEPTIDES AND  
POLYNUCLEOTIDES  
Applicants: Tianhua Hu  
Docket No.: HYS-46CIP  
24/32



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      470      480      490      500      510      520
SEQ 62 GGGGAGATGGGCAGCCCCGGCGCCCCGTGCCAGAAGCGCTTCTTCGCCTTCTCAGTGGGC
      .....
SEQ 66 GGGGAGATGGGCAGCCCCGGCGCCCCGTGCCAGAAGCGCTTCTTCGCCTTCTCAGTGGGC
      460      470      480      490      500      510

      530      540      550      560      570      580
SEQ 62 CGCAAGACGGCCCTGCACAGCGGCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTT
      .....
SEQ 66 CGCAAGACGGCCCTGCACAGCGGCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTT
      520      530      540      550      560      570

      590      600      610      620      630      640
SEQ 62 GTGAACCTTGATGGGTGCTTTGACATGGCGACCGGCCAGTTTGCTGCTCCCCTGCGTGGC
      .....
SEQ 66 GTGAACCTTGATGGGTGCTTTGACATGGCGACCGGCCAGTTTGCTGCTCCCCTGCGTGGC
      580      590      600      610      620      630

      650      660      670      680      690      700
SEQ 62 ATCTACTTCTTCAGCCTCAATGTGCACAGCTGGAATTACAAGGAGACGTACGTGCACATT
      .....
SEQ 66 ATCTACTTCTTCAGCCTCAATGTGCACAGCTGGAATTACAAGGAGACGTACGTGCACATT
      640      650      660      670      680      690

      710      720      730      740      750      760
SEQ 62 ATGCATAACCAGAAAGAGGCTGTTCATCCTGTACGCGCAGCCCAGCGAGCGCAGCATCATG
      .....
SEQ 66 ATGCATAACCAGAAAGAGGCTGTTCATCCTGTACGCGCAGCCCAGCGAGCGCAGCATCATG
      700      710      720      730      740      750

      770      780      790      800      810      820
SEQ 62 CAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACCGCGTCTGGGTGCGGCTCTTC
      .....
SEQ 66 CAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACCGCGTCTGGGTGCGGCTCTTC
      760      770      780      790      800      810

      830      840      850      860      870      880
SEQ 62 AAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTTCGACACCTACATCACCTTCAGC
      .....
SEQ 66 AAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTTCGACACCTACATCACCTTCAGC
      820      830      840      850      860      870

      890      900      910      920      930      940
SEQ 62 GGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGGGCCACCTCCCGGCTGGAGA
      .....
SEQ 66 GGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGGGCCACCTCCCGGCTGGAGA
      880      890      900      910      920      930

      950      960      970      980      990      1000
SEQ 62 GCTCAGGTGCTGGTCCCCTGCCCTGCAGGGCTCAGTTTGCACTGCTGTGAAGCAGGAAGG
      .....
SEQ 66 GCTCAGGTGCTGGTCCCCTGCCCTGCAGGGCTCAGTTTGCACTGCTGTGAAGCAGGAAGG
      940      950      960      970      980      990

```

FIGURE 17B

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1010      1020      1030      1040      1050      1060
SEQ 62 CCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGACCTGCTTCTATCTTGGCTGCCA
      .....
SEQ 66 CCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGACCTGCTTCTATCTTGGCTGCCA
      1000      1010      1020      1030      1040      1050

1070      1080      1090      1100      1110      1120
SEQ 62 TCATCCCTCCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAGAAGCTT
      .....
SEQ 66 TCATCCCTCCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAGAAGCTT
      1060      1070      1080      1090      1100      1110

1130      1140      1150      1160      1170      1180
SEQ 62 GCTAACCTAAATATTCTAGAACTTTCCCAGCCTCGTAGCCCAGCACTTCTCAAACCTTGGA
      .....
SEQ 66 GCTAACCTAAATATTCTAGAACTTTCCCAGCCTCGTAGCCCAGCACTTCTCAAACCTTGGA
      1120      1130      1140      1150      1160      1170

1190      1200      1210      1220      1230      1240
SEQ 62 AATGCATGCGAATCACCCGGGGTTTCGTGTTAAATGCAGATTCTGACTCAGCAGGTCTGAG
      .....
SEQ 66 AATGCATGCGAATCACCCGGGGTTTCGTGTTAAATGCAGATTCTGACTCAGCAGGTCTGAG
      1180      1190      1200      1210      1220      1230

1250      1260      1270      1280      1290      1300
SEQ 62 TGGGTCCAGGATTCTGTGTTTCTCATATGTTCCCTGGGTGATGCTGATGGGGTCAGTCTAT
      .....
SEQ 66 TGGGTCCAGGATTCTGTGTTTCTCATATGTTCCCTGGGTGATGCTGATGGGGTCAGTCTAT
      1240      1250      1260      1270      1280      1290

1310      1320      1330      1340      1350      1360
SEQ 62 GAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACA
      .....
SEQ 66 GAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACA
      1300      1310      1320      1330      1340      1350

1370      1380      1390      1400      1410      1420
SEQ 62 TTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTCTTGAGACAGAGT
      .....
SEQ 66 TTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTCTTGAGACAGAGT
      1360      1370      1380      1390      1400      1410

1430      1440      1450      1460      1470      1480
SEQ 62 CTTGCTCTGTTGCCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTGCAACCTCTGC
      .....
SEQ 66 CTTGCTCTGTTGCCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTGCAACCTCTGC
      1420      1430      1440      1450      1460      1470

1490      1500      1510      1520      1530      1540
SEQ 62 CTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTACAGGCGCC
      .....
SEQ 66 CTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTACAGGCGCC
      1480      1490      1500      1510      1520      1530

```

FIGURE 17C

```

1550      1560      1570      1580      1590      1600
SEQ 62 TGCTACCATGCCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCATATTGGC
      :
      :
      :
SEQ 66 TGCTACCATGCCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCATATTGGC
      1540      1550      1560      1570      1580      1590

1610      1620      1630      1640      1650      1660
SEQ 62 CAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCGCCCTCGGCCTCTCAAAATGCT
      :
      :
      :
SEQ 66 CAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCGCCCTCGGCCTCTCAAAATGCT
      1600      1610      1620      1630      1640      1650

1670      1680      1690      1700      1710      1720
SEQ 62 GGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATTCTCTCATC
      :
      :
      :
SEQ 66 GGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATTCTCTCATC
      1660      1670      1680      1690      1700      1710

1730      1740      1750      1760      1770      1780
SEQ 62 CCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGC
      :
      :
      :
SEQ 66 CCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGC
      1720      1730      1740      1750      1760      1770

1790      1800      1810      1820      1830      1840
SEQ 62 CTGCACCACTGCAGCCACCGTTCAATTTATTCATTCAATTAACACTGAGCACTCACTCTGT
      :
      :
      :
SEQ 66 CTGCACCACTGCAGCCACCGTTCAATTTATTCATTCAATTAACACTGAGCACTCACTCTGT
      1780      1790      1800      1810      1820      1830

1850      1860      1870      1880      1890      1900
SEQ 62 GCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGACT
      :
      :
      :
SEQ 66 GCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGACT
      1840      1850      1860      1870      1880      1890

1910      1920      1930      1940      1950      1960
SEQ 62 GGCCAGTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCT
      :
      :
      :
SEQ 66 GGCCAGTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCT
      1900      1910      1920      1930      1940      1950

1970      1980      1990      2000      2010      2020
SEQ 62 CATGGGGGCCTGTGTTCTGGGTGTTTCAGGTGCTGCTGGTCCTCCATTACCCACTGCTCCC
      :
      :
      :
SEQ 66 CATGGGGGCCTGTGTTCTGGGTGTTTCAGGTGCTGCTGGTCCTCCATTACCCACTGCTCCC
      1960      1970      1980      1990      2000      2010

2030      2040      2050      2060      2070      2080
SEQ 62 CAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCCTTCCCGTTCCCTCATC
      :
      :
      :
SEQ 66 CAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCCTTCCCGTTCCCTCATC
      2020      2030      2040      2050      2060      2070

```

FIGURE 17D

```

      2090      2100      2110      2120      2130      2140
SEQ 62 CACCTGCCCAGTGCCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTT
      .....
SEQ 66 CACCTGCCCAGTGCCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTT
      2080      2090      2100      2110      2120      2130

      2150      2160      2170      2180      2190      2200
SEQ 62 CTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGAA
      .....
SEQ 66 CTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGAA
      2140      2150      2160      2170      2180      2190

      2210      2220      2230      2240      2250      2260
SEQ 62 TGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCC
      .....
SEQ 66 TGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCC
      2200      2210      2220      2230      2240      2250

      2270      2280      2290      2300      2310      2320
SEQ 62 CTCCTCACTGGGATCCCCCTTCCTGCCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTC
      .....
SEQ 66 CTCCTCACTGGGATCCCCCTTCCTGCCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTC
      2260      2270      2280      2290      2300      2310

      2330      2340      2350      2360      2370      2380
SEQ 62 CCTTCCACCAAAGTCATCTGAAC TTCCGTTTCCCAGGGCTCCAGCTGCCCTCAGACAC
      .....
SEQ 66 CCTTCCACCAAAGTCATCTGAAC TTCCGTTTCCCAGGGCTCCAGCTGCCCTCAGACAC
      2320      2330      2340      2350      2360      2370

      2390      2400      2410      2420      2430      2440
SEQ 62 TGATGTCTGTCCCCAGGTGCTCTCTGCCCCCTCATGCCCCCTCTACCGGCCAGTGCCCCG
      .....
SEQ 66 TGATGTCTGTCCCCAGGTGCTCTCTGCCCCCTCATGCCCCCTCTACCGGCCAGTGCCCCG
      2380      2390      2400      2410      2420      2430

      2450      2460      2470      2480      2490      2500
SEQ 62 ACTCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCC
      .....
SEQ 66 ACTCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCC
      2440      2450      2460      2470      2480      2490

      2510      2520      2530      2540      2550      2560
SEQ 62 TCCTCCGGCCTGGTGCTGCCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAG
      .....
SEQ 66 TCCTCCGGCCTGGTGCTGCCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAG
      2500      2510      2520      2530      2540      2550

      2570      2580      2590      2600      2610      2620
SEQ 62 GCTTTAGAGCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCG
      .....
SEQ 66 GCTTTAGAGCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCG
      2560      2570      2580      2590      2600      2610

```

FIGURE 17E

```

      2630      2640      2650      2660      2670      2680
SEQ 62 TTTCTTCTTCCAGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCT
      :
      :
SEQ 66 TTTCTTCTTCCAGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCT
      2620      2630      2640      2650      2660      2670

      2690      2700      2710      2720      2730      2740
SEQ 62 GCCCTTCTCCCCAGAGGGAGGCGGCCTCCGCCCATTGGTGCTCATGCAGACTCTGGGGCT
      :
      :
SEQ 66 GCCCTTCTCCCCAGAGGGAGGCGGCCTCCGCCCATTGGTGCTCATGCAGACTCTGGGGCT
      2680      2690      2700      2710      2720      2730

      2750      2760      2770      2780      2790      2800
SEQ 62 GAGGTGCCCCGGGGGGTGGTGTCTGCTGCTCACAGCCGAGGAGCCGTGGCTCCATGGCCA
      :
      :
SEQ 66 GAGGTGCCCCGGGGGGTGGTGTCTGCTGCTCACAGCCGAGGAGCCGTGGCTCCATGGCCA
      2740      2750      2760      2770      2780      2790

      2810      2820      2830      2840      2850      2860
SEQ 62 GATGACGGAACAGGGTCTGACCAAGTGCCAGGAAGACCTGTGCTATAAACCACCCTGCC
      :
      :
SEQ 66 GATGACGGAACAGGGTCTGACCAAGTGCCAGGAAGACCTGTGCTATAAACCACCCTGCC
      2800      2810      2820      2830      2840      2850

      2870      2880      2890      2900      2910      2920
SEQ 62 TGATCCTGCCCCTGCTGACCCCGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTG
      :
      :
SEQ 66 TGATCCTGCCCCTGCTGACCCCGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTG
      2860      2870      2880      2890      2900      2910

      2930      2940
SEQ 62 TCTCCTCAAAAAAAAAA
      :
      :
SEQ 66 TCTCCTCAAAAAAAAAA
      2920

```

FIGURE 17F

BLASTP AMINO ACID SEQUENCE ALIGNMENT OF HIBERNATION  
PROTEIN-LIKE CDCP POLYPEPTIDE (SEQ ID NO: 68) AND  
CHIPMUNK hp-20 PRECURSOR (SEQ ID NO: 79)

>gi|1170339|sp|Q06575|HP20\_TAMSI Hibernation-associated plasma protein HP-20  
precursor [Tamias sibiricus]  
Length = 196

Score = 154 bits (390), Expect = 6e-37

Identities = 77/153 (50%), Positives = 102/153 (66%), Gaps = 7/153 (4%)

```
SEQ 68: 20  PGAPGLPQYTGEISEMTKCPCPDIERSAFTVKLSGKLPLPFKPIIFTGVLYNAQRDLKEA 79
              PGA G P   G      KCPC   ERSFTVK SG+LP P +P++FT VLYN QRDLE+
SEQ 79: 48  PGAAGRPGDPGPKGPSVKCPCR--ERSFTVKFSGRLPPPSEPVVFTVLYNTQRDLKES 105

SEQ 68: 80  MGVFACRVPGNYSSFDVELHHCKPFQHAVKLGLMKNSTQVLEKEANAEDNYRHVFGTVV 139
              GVF C  PGN+ SFDVEL+HCK      VK+GLMKN QV+EK   +++ Y +  G ++
SEQ 79: 106 TGVFNCVEPGNYHFSFDVELYHCK-----VKIGLMKNHIQVMEKHQLSKNEYENASGAMI 160

SEQ 68: 140 LQLMMGDRVWLKSKLEAKENEKGLIQSVFCGYL 172
              + L  GD+VWL++ +E +E ++  +   F G+L
SEQ 79: 161 MPLRQGDQVWLEADVETEEPDQAKVVIYFSGFL 193
```

FIGURE 18

Figure 19A

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